



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

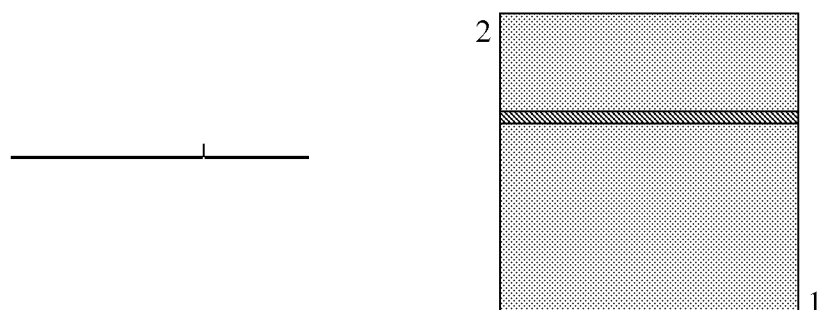
Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: Mismatch: gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ View option
Masking character option Masking color option
☐ Show CDS translation

Sequence 1: lcl|1 SEQ ID NO:101 from Pompejus et al.
Length = 861 (1 .. 861)

Sequence 2: gi|14041139|Sequence 7067 from Patent EP1108790
Length = 349980 (1 .. 349980)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

NOTE: If protein translation is reversed, please repeat the search with reverse strand of the query sequence.

Score = 1656 bits (861), Expect = 0.0
Identities = 861/861 (100%), Gaps = 0/861 (0%)
Strand=Plus/Minus

Query	1	GAGTTGGCCGATTACATCCCGGAACTAAAATCTGCGGACCCAAACCCGCTGGCAGTAGCC	60
Sbjct	227662	GAGTTGGCCGATTACATCCCGGAACTAAAATCTGCGGACCCAAACCCGCTGGCAGTAGCC	227603
Query	61	CTGTGCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCATG	120
Sbjct	227602	CTGTGCACCGTTAACGGACACATCTACAGCGCAGGCGATGACGACATCGAATTCACCATG	227543
Query	121	CAAAGTATTTCCAAGCCATTTGCCTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAG	180
Sbjct	227542	CAAAGTATTTCCAAGCCATTTGCCTACGCACTCGCACTCCAAGAATGCGGCTTTGATGAG	227483
Query	181	GTCTCTGCATCCGTGGCCTTGGAGCCCTCCGGTGAGGCCTTCAACGAACCTTCCCTCGAC	240
Sbjct	227482	GTCTCTGCATCCGTGGCCTTGGAGCCCTCCGGTGAGGCCTTCAACGAACCTTCCCTCGAC	227423
Query	241	GGCGAAAACCGCCCCATGAACCCCATGATCAACGCCGGCGCGATCGCCATCAACCAGCTG	300

Sbjct	227422	GGCGAAAACCGCCCCATGAACCCCATGATCAACGCCGGCGCGATCGCCATCAACCAGCTG	227363
Query	301	ATCAACGGCTCCGATTCCACCGTGGAAGACCGCGTGGAATAATCCGACACTACTTCTCT	360
Sbjct	227362	ATCAACGGCTCCGATTCCACCGTGGAAGACCGCGTGGAATAATCCGACACTACTTCTCT	227303
Query	361	GAAGTTGCTGGACGCGAAGTCAACATCGACCGCGTGCTTGCCGAATCCGAAGTCCGCGGC	420
Sbjct	227302	GAAGTTGCTGGACGCGAAGTCAACATCGACCGCGTGCTTGCCGAATCCGAAGTCCGCGGC	227243
Query	421	GCCGACCGCAACCTCTCCATCGCCACATGCTGCGCAATTACGGCGTCATCGAAGACGAA	480
Sbjct	227242	GCCGACCGCAACCTCTCCATCGCCACATGCTGCGCAATTACGGCGTCATCGAAGACGAA	227183
Query	481	GCCCACGACGCCGTCTCAGCTACACGCTGCAATGCGCCATCAAAGTAACCACGCGCGAC	540
Sbjct	227182	GCCCACGACGCCGTCTCAGCTACACGCTGCAATGCGCCATCAAAGTAACCACGCGCGAC	227123
Query	541	CTCGCAGTCATGACCGCCACGCTCGCCGCCGGCGGCACACACCCAATTACCGGCAAGAAG	600
Sbjct	227122	CTCGCAGTCATGACCGCCACGCTCGCCGCCGGCGGCACACACCCAATTACCGGCAAGAAG	227063
Query	601	CTTCTCGACGCCCGCGTCTGCCGCCTCACCTCTCCGTATGGCTTCAGCAGGCATGTAC	660
Sbjct	227062	CTTCTCGACGCCCGCGTCTGCCGCCTCACCTCTCCGTATGGCTTCAGCAGGCATGTAC	227003
Query	661	GACGAGGCAGGGCAGTGGCTCTCCACCGTAGGCATCCCCGCGAAATCAGGAGTCGCCGGC	720
Sbjct	227002	GACGAGGCAGGGCAGTGGCTCTCCACCGTAGGCATCCCCGCGAAATCAGGAGTCGCCGGC	226943
Query	721	GGACTCATCGGCATTCTGCCAGGTGAGTGGGCATCGCCACATTTTCCCCACGCCTGAAC	780
Sbjct	226942	GGACTCATCGGCATTCTGCCAGGTGAGTGGGCATCGCCACATTTTCCCCACGCCTGAAC	226883
Query	781	CCCAAAGGCAACAGCGTGC GCGCGTAAAAATATTCAAACAGCTTTCCGACGACATGGGC	840
Sbjct	226882	CCCAAAGGCAACAGCGTGC GCGCGTAAAAATATTCAAACAGCTTTCCGACGACATGGGC	226823
Query	841	CTCCACCTCATGTCCACCGAG	861
Sbjct	226822	CTCCACCTCATGTCCACCGAG	226802

CPU time: 0.05 user secs. 0.05 sys. secs 0.10 total secs.